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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/718,321A

DATE: 07/10/2002 P.6  
TIME: 10:44:58

Input Set : D:\Cura-99.app

Output Set: N:\CRF3\07102002\I718321A.raw

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4 <110> APPLICANT: Shimkets, Richard A.
5   Leach, Martin D.
7 <120> TITLE OF INVENTION: NUCLEIC ACIDS CONTAINING SINGLE NUCLEIC ACID POLYMORPHISMS
AND METHODS OF
8   USE THEREOF
10 <130> FILE REFERENCE: 15966-599
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/718,321A
C--> 12 <141> CURRENT FILING DATE: 2002-06-20
12 <150> PRIOR APPLICATION NUMBER: 60/163,783
13 <151> PRIOR FILING DATE: 1999-11-24
15 <160> NUMBER OF SEQ ID NOS: 1468
17 <170> SOFTWARE: CuraGen Patent Formatter Version 0.9
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20 <211> LENGTH: 51
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
24 <220> FEATURE:
25 <221> NAME/KEY: allele
26 <222> LOCATION: (26)...(0)
27 <223> OTHER INFORMATION: single nucleotide polymorphism
29 <221> NAME/KEY: misc_feature
30 <222> LOCATION: (0)...(0)
31 <223> OTHER INFORMATION: Accession number cg43921971
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37 <211> LENGTH: 51
38 <212> TYPE: DNA
39 <213> ORGANISM: Homo sapiens
41 <220> FEATURE:
42 <221> NAME/KEY: allele
43 <222> LOCATION: (26)...(0)
44 <223> OTHER INFORMATION: single nucleotide polymorphism
46 <221> NAME/KEY: misc_feature
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48 <223> OTHER INFORMATION: Accession number cg43336508
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54 <211> LENGTH: 50
55 <212> TYPE: DNA
56 <213> ORGANISM: Homo sapiens
58 <220> FEATURE:
59 <221> NAME/KEY: allele

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61 <223> OTHER INFORMATION: single nucleotide polymorphism
63 <221> NAME/KEY: misc_feature
64 <222> LOCATION: (25)...(26)
65 <223> OTHER INFORMATION: Nucleotide deleted between bases 25 and 26
W--> 67 <221> misc_feature
68 <222> LOCATION: (0)...(0)
69 <223> OTHER INFORMATION: Accession number cg43314087
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75 <211> LENGTH: 50
76 <212> TYPE: DNA
77 <213> ORGANISM: Homo sapiens
79 <220> FEATURE:
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82 <223> OTHER INFORMATION: single nucleotide polymorphism
84 <221> NAME/KEY: misc_feature
85 <222> LOCATION: (25)...(26)
86 <223> OTHER INFORMATION: Nucleotide deleted between bases 25 and 26
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89 <222> LOCATION: (0)...(0)
90 <223> OTHER INFORMATION: Accession number cg43314087
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96 <211> LENGTH: 50
97 <212> TYPE: DNA
98 <213> ORGANISM: Homo sapiens
100 <220> FEATURE:
101 <221> NAME/KEY: allele
102 <222> LOCATION: (26)...(0)
103 <223> OTHER INFORMATION: single nucleotide polymorphism
105 <221> NAME/KEY: misc_feature
106 <222> LOCATION: (25)...(26)
107 <223> OTHER INFORMATION: Nucleotide deleted between bases 25 and 26
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110 <222> LOCATION: (0)...(0)
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116 <210> SEQ ID NO: 6
117 <211> LENGTH: 50
118 <212> TYPE: DNA
119 <213> ORGANISM: Homo sapiens
121 <220> FEATURE:
122 <221> NAME/KEY: allele
123 <222> LOCATION: (26)...(0)

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Input Set : D:\Cura-99.app

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124 <223> OTHER INFORMATION: single nucleotide polymorphism
126 <221> NAME/KEY: misc_feature
127 <222> LOCATION: (25)...(26)
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131 <222> LOCATION: (0)...(0)
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140 <213> ORGANISM: Homo sapiens
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145 <223> OTHER INFORMATION: single nucleotide polymorphism
147 <221> NAME/KEY: misc_feature
148 <222> LOCATION: (0)...(0)
149 <223> OTHER INFORMATION: Accession number cg43988460
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156 <212> TYPE: DNA
157 <213> ORGANISM: Homo sapiens
159 <220> FEATURE:
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161 <222> LOCATION: (26)...(0)
162 <223> OTHER INFORMATION: single nucleotide polymorphism
164 <221> NAME/KEY: misc_feature
165 <222> LOCATION: (25)...(26)
166 <223> OTHER INFORMATION: Nucleotide deleted between bases 25 and 26
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169 <222> LOCATION: (0)...(0)
170 <223> OTHER INFORMATION: Accession number cg43982945
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173 gacacatgtc aggctggggc agcagcactc tgatcagcac caggtcccga 50
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176 <211> LENGTH: 50
177 <212> TYPE: DNA
178 <213> ORGANISM: Homo sapiens
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181 <221> NAME/KEY: allele
182 <222> LOCATION: (26)...(0)
183 <223> OTHER INFORMATION: single nucleotide polymorphism
185 <221> NAME/KEY: misc_feature
186 <222> LOCATION: (25)...(26)
187 <223> OTHER INFORMATION: Nucleotide deleted between bases 25 and 26

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Input Set : D:\Cura-99.app

Output Set: N:\CRF3\07102002\I718321A.raw

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W--> 189 <221> misc_feature
190 <222> LOCATION: (0)...(0)
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198 <212> TYPE: DNA
199 <213> ORGANISM: Homo sapiens
201 <220> FEATURE:
202 <221> NAME/KEY: allele
203 <222> LOCATION: (26)...(0)
204 <223> OTHER INFORMATION: single nucleotide polymorphism
206 <221> NAME/KEY: misc_feature
207 <222> LOCATION: (25)...(26)
208 <223> OTHER INFORMATION: Nucleotide deleted between bases 25 and 26
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211 <222> LOCATION: (0)...(0)
212 <223> OTHER INFORMATION: Accession number cg43321451
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218 <211> LENGTH: 51
219 <212> TYPE: DNA
220 <213> ORGANISM: Homo sapiens
222 <220> FEATURE:
223 <221> NAME/KEY: allele
224 <222> LOCATION: (26)...(0)
225 <223> OTHER INFORMATION: single nucleotide polymorphism
227 <221> NAME/KEY: misc_feature
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229 <223> OTHER INFORMATION: Accession number cg43933757
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232 tcattctccct gcaacctccg cctcccgggt tcaagcgatt cttgtgcctc a 51
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235 <211> LENGTH: 51
236 <212> TYPE: DNA
237 <213> ORGANISM: Homo sapiens
239 <220> FEATURE:
240 <221> NAME/KEY: allele
241 <222> LOCATION: (26)...(0)
242 <223> OTHER INFORMATION: single nucleotide polymorphism
244 <221> NAME/KEY: misc_feature
245 <222> LOCATION: (0)...(0)
246 <223> OTHER INFORMATION: Accession number cg43933757
W--> 248 <400> 12
249 ccgcctcctg ggttcaagcg attctcgtgc ctcagcctcc caagcagctg g 51
251 <210> SEQ ID NO: 13
252 <211> LENGTH: 51

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## RAW SEQUENCE LISTING

DATE: 07/10/2002

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TIME: 10:44:58

Input Set : D:\Cura-99.app

Output Set: N:\CRF3\07102002\I718321A.raw

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253 <212> TYPE: DNA
254 <213> ORGANISM: Homo sapiens
256 <220> FEATURE:
257 <221> NAME/KEY: allele
258 <222> LOCATION: (26)...(0)
259 <223> OTHER INFORMATION: single nucleotide polymorphism
261 <221> NAME/KEY: misc_feature
262 <222> LOCATION: (0)...(0)
263 <223> OTHER INFORMATION: Accession number cg43933757
W--> 265 <400> 13
266 tccaactcct gacctcaggt aatccacctg ccttggcctc ccaaagtgt g 51
268 <210> SEQ ID NO: 14
269 <211> LENGTH: 50
270 <212> TYPE: DNA
271 <213> ORGANISM: Homo sapiens
273 <220> FEATURE:
274 <221> NAME/KEY: allele
275 <222> LOCATION: (26)...(0)
276 <223> OTHER INFORMATION: single nucleotide polymorphism
278 <221> NAME/KEY: misc_feature
279 <222> LOCATION: (25)...(26)
280 <223> OTHER INFORMATION: Nucleotide deleted between bases 25 and 26
W--> 282 <221> misc_feature
283 <222> LOCATION: (0)...(0)
284 <223> OTHER INFORMATION: Accession number cg42185571
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287 cttagctcta cgatttaa at ccatggtcca agggggaaaa catattatat 50
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290 <211> LENGTH: 50
291 <212> TYPE: DNA
292 <213> ORGANISM: Homo sapiens
294 <220> FEATURE:
295 <221> NAME/KEY: allele
296 <222> LOCATION: (26)...(0)
297 <223> OTHER INFORMATION: single nucleotide polymorphism
299 <221> NAME/KEY: misc_feature
300 <222> LOCATION: (25)...(26)
301 <223> OTHER INFORMATION: Nucleotide deleted between bases 25 and 26
W--> 303 <221> misc_feature
304 <222> LOCATION: (0)...(0)
305 <223> OTHER INFORMATION: Accession number cg42185571
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310 <210> SEQ ID NO: 16
311 <211> LENGTH: 51
312 <212> TYPE: DNA
313 <213> ORGANISM: Homo sapiens
315 <220> FEATURE:
316 <221> NAME/KEY: allele

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/718,321A

DATE: 07/10/2002  
TIME: 10:44:59

Input Set : D:\Cura-99.app  
Output Set: N:\CRF3\07102002\I718321A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:120; N Pos. 1

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 7

## VERIFICATION SUMMARY

DATE: 07/10/2002

PATENT APPLICATION: US/09/718,321A

TIME: 10:44:59

Input Set : D:\Cura-99.app

Output Set: N:\CRF3\07102002\I718321A.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:33 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1  
L:50 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2  
L:67 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3  
L:71 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3  
L:88 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4  
L:92 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4  
L:109 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5  
L:113 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5  
L:130 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6  
L:134 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6  
L:151 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7  
L:168 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8  
L:172 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8  
L:189 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:9  
L:193 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:9  
L:210 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:10  
L:214 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:10  
L:231 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11  
L:248 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:12  
L:265 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:13  
L:282 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:14  
L:286 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:14  
L:303 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15  
L:307 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15  
L:324 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:16  
L:341 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:17  
L:358 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:18  
L:375 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:19  
L:392 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:20  
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L:451 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:23  
L:468 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:24  
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L:506 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:26  
L:523 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:27  
L:540 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:28  
L:557 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:29  
L:574 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:30  
L:591 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:31  
L:608 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:32  
L:625 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:33  
L:642 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:34

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TIME: 10:44:59

Input Set : D:\Cura-99.app

Output Set: N:\CRF3\07102002\I718321A.raw

L:677 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:36  
L:730 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:39  
L:765 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:41  
L:769 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:41  
L:2186 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:120 after pos.:0